

FIGURE 1

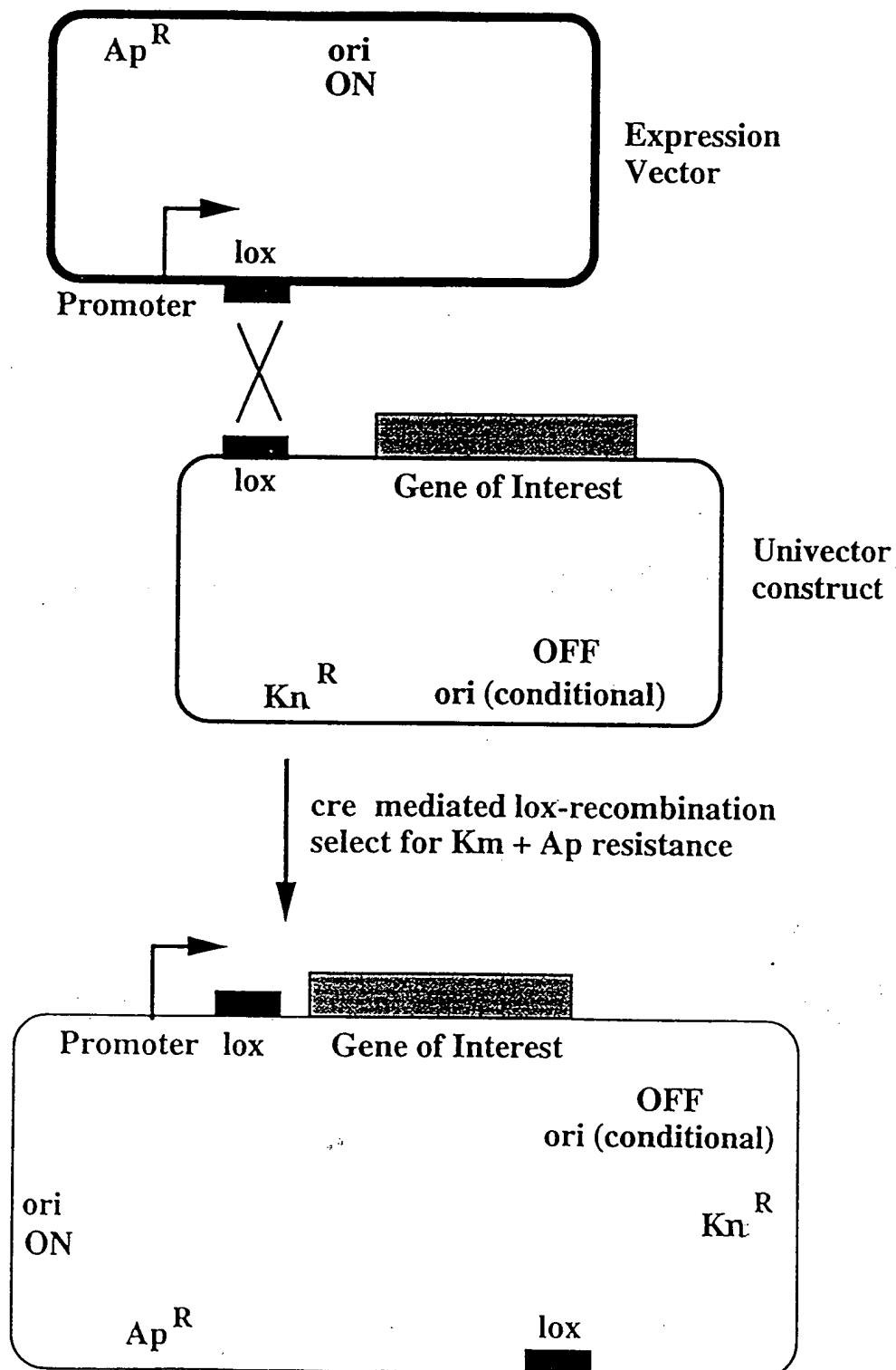
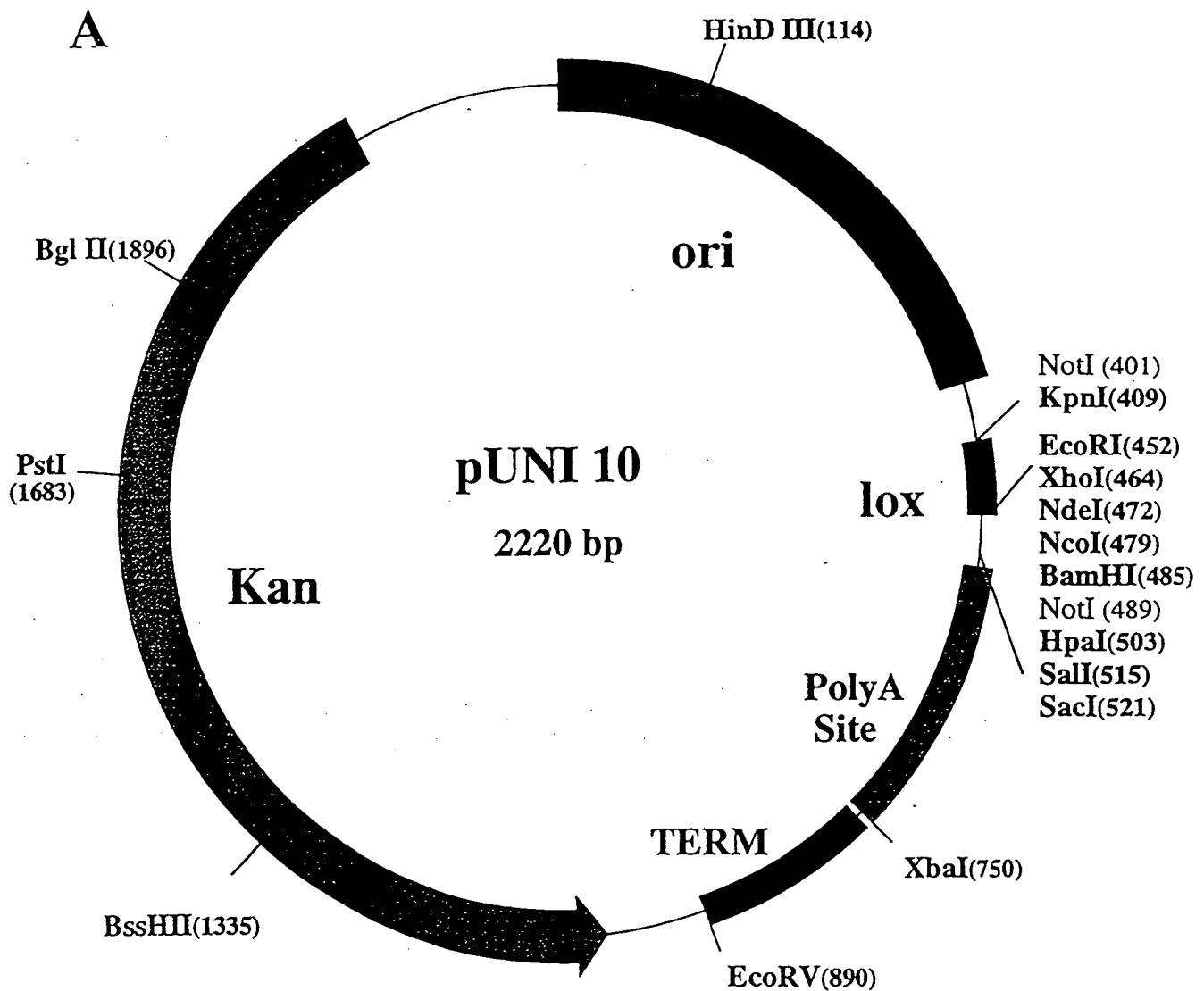


FIGURE 2



B

(401) NotI KpnI LOX

GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TCT

EcoRI SmaI XhoI NdeI NcoI BamHI NotI

GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG GGG ATC CGC GGC CGC

HpaI SalI SacI

AAT TGT TAA CAG ATC CGT CGA CGA GCT CGC TA (530)

FIGURE 3

Construction of pGst-lox:

A

Linker: C ATG GCT ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG
 CGA TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG
 NcoI BamHI

B

MCS: CAT ATG CCC ATG GCT CGA GGA TCC GAA TTC
 NdeI NcoI XhoI EcoRI BamHI

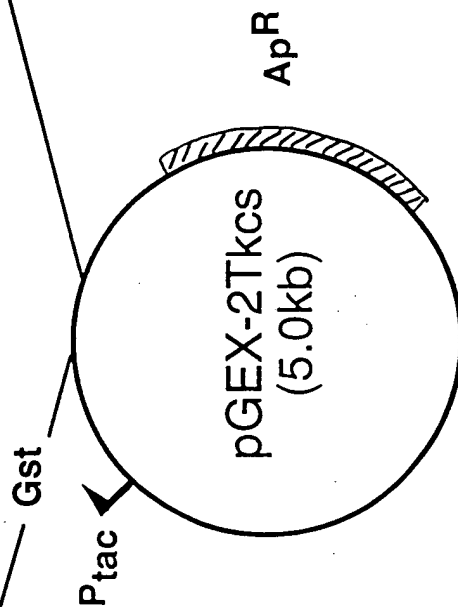


FIGURE 4

Construction of pVL1392-lox:

A

Linker: GG CCG GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TG
 C CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT AC CTAG
 NotI BamHI

B

MCS: BglII/PstI/NotI/XmaI/EcoRI/XbaI/SmaI/BamHI

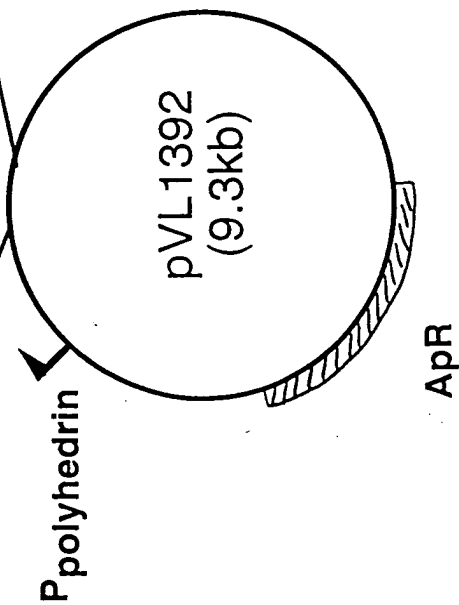


FIGURE 5

Construction of pGAP24-lox:

A

Linker: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC
 CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT ACG CCGG
 XhoI NotI

B

MCS: XhoI/BclI/NotI/EagI/StyI/AflII

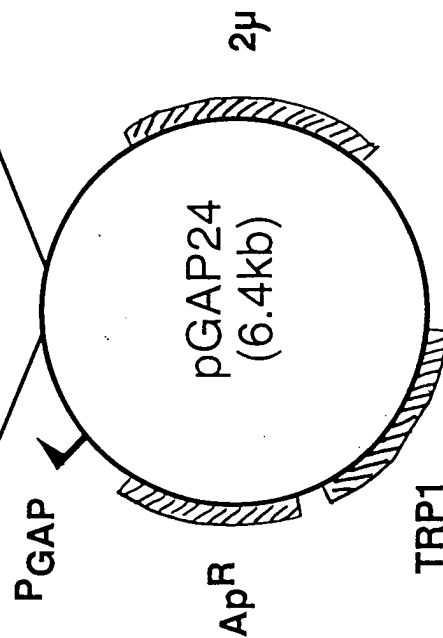


FIGURE 6

Construction of pGAL14-lox:

A

Linker: T CGA GAC GTC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TGC TGC
 CTG CAG TAT TGA AGC ATA TCG TAT GTA ATA TGC TTC AAT ACG CCGG
 XhoI NotI

B

MCS: SalI/ClaI/PstI/SmaI/XmaI/SpeI/NotI/EagI/SacII/SacI

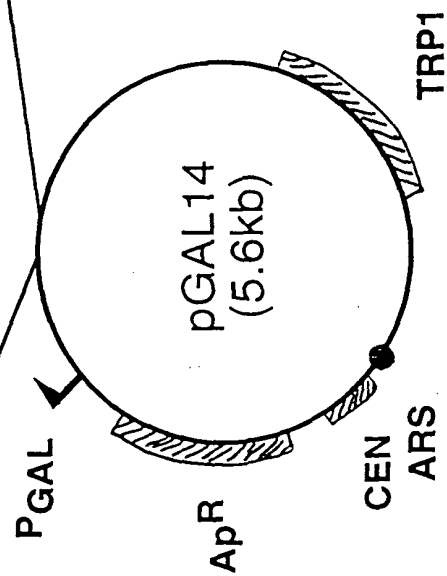


FIGURE 7

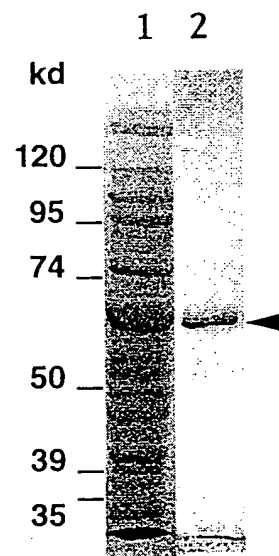


FIGURE 8

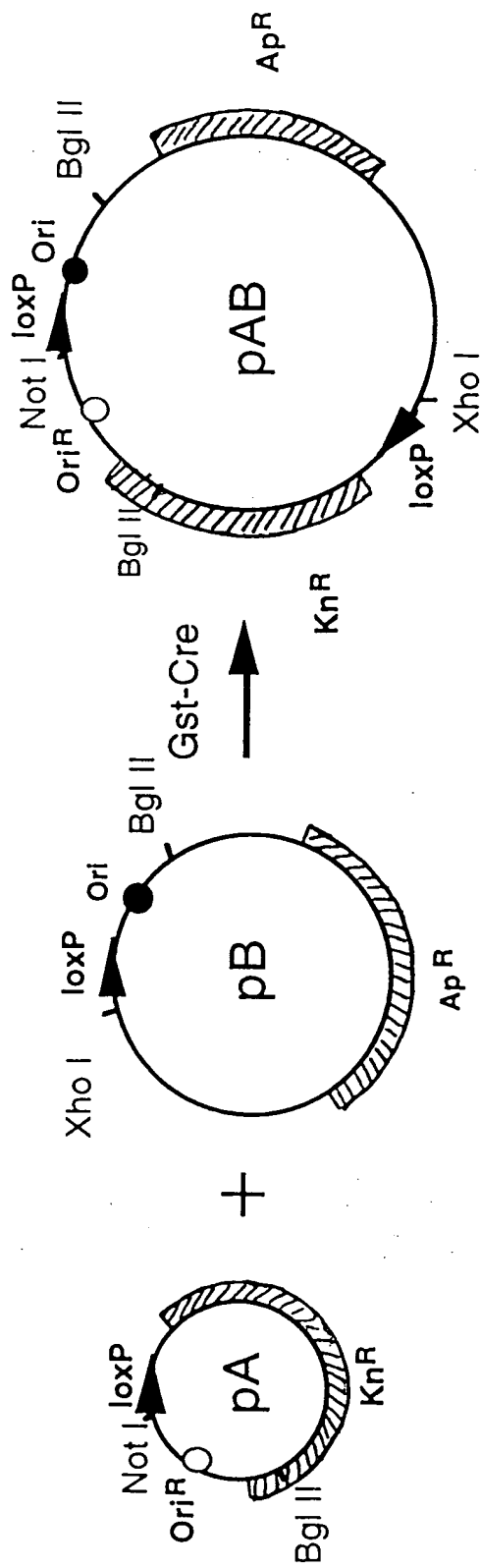
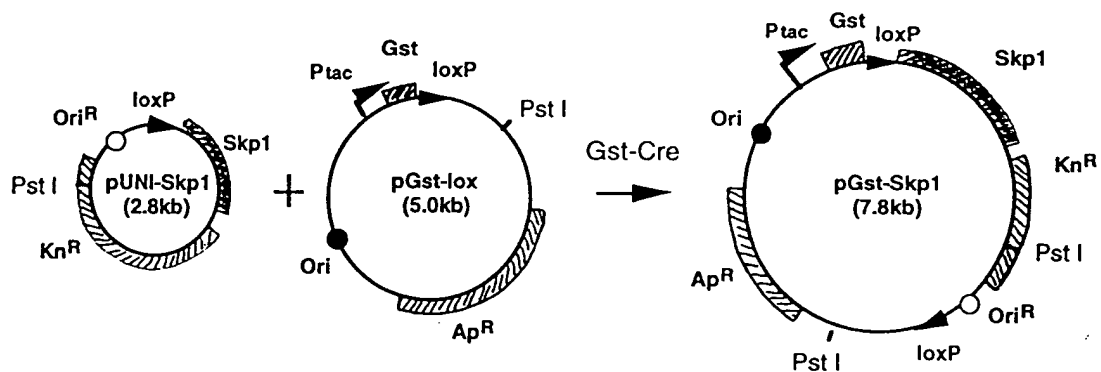


FIGURE 9

A



B

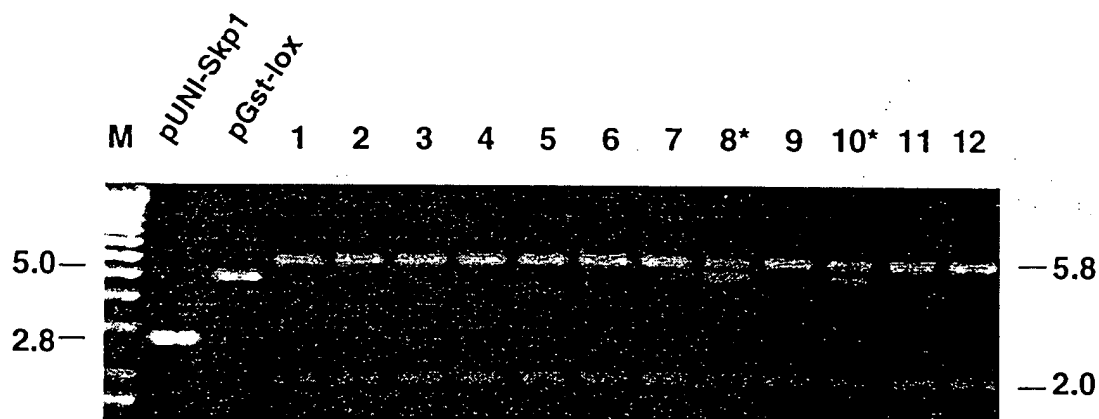
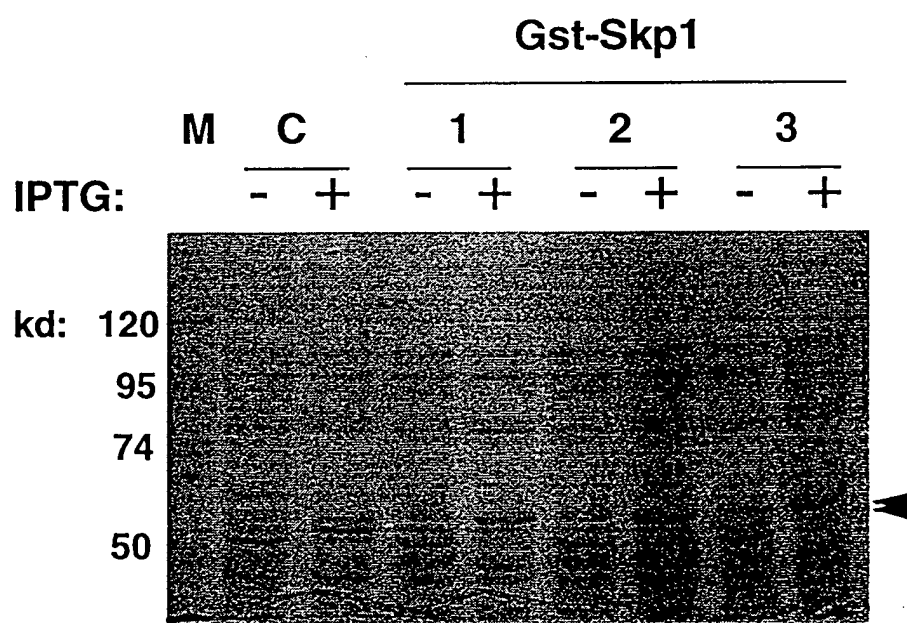


FIGURE 10

A



B

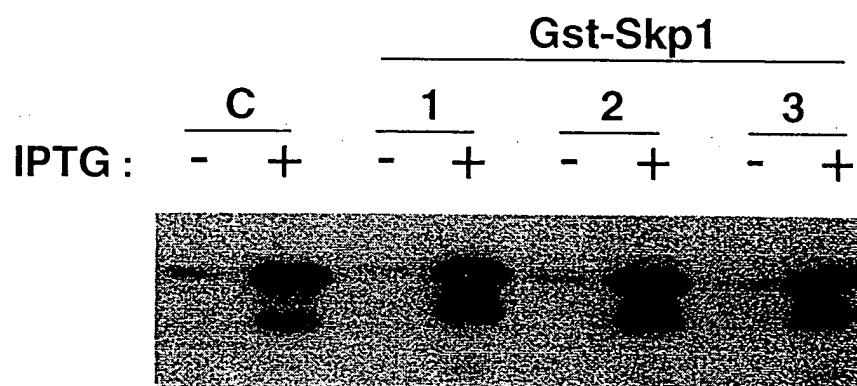


FIGURE 11

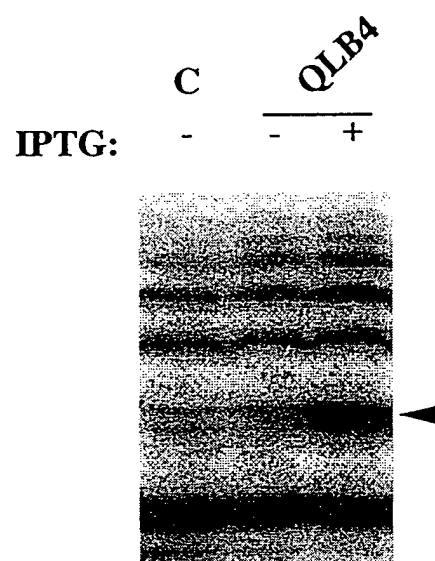
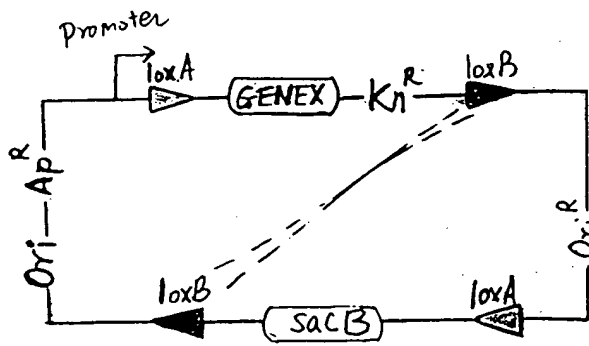
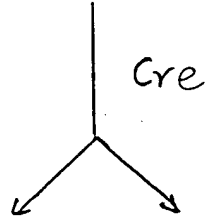
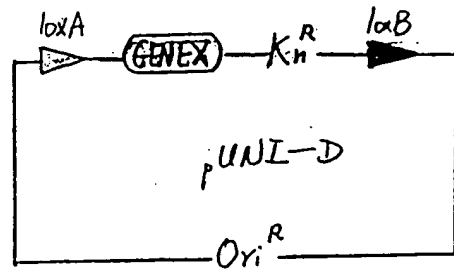
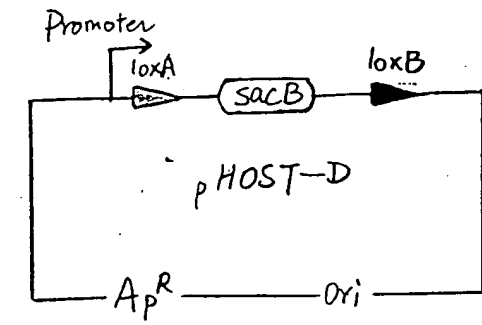


FIGURE 12



or

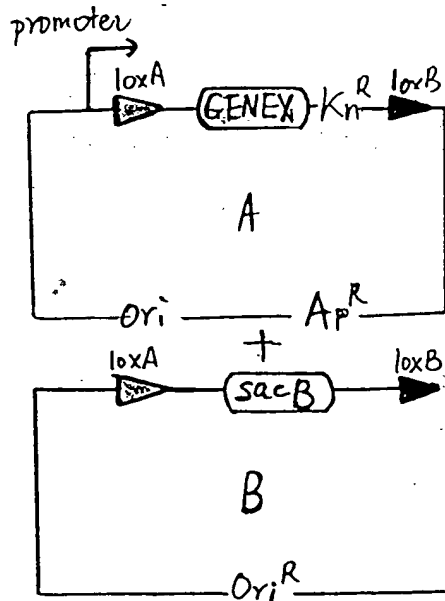
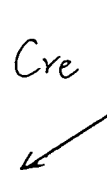
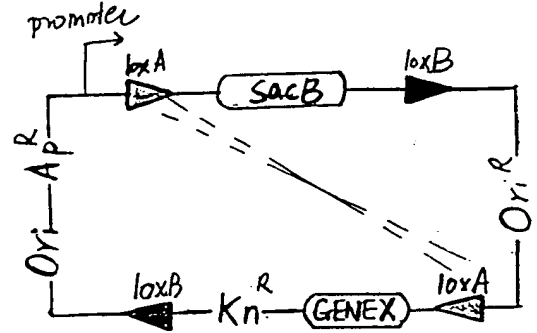


FIGURE 13

loxP: ATAACTTCGTATA GCATACAT TATACGAAGTTAT
 1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T **C**
 | |
 loxP2: ATA**A**ACT**T**TCGTATA GCATACAT TATACGAAGTTAT
 1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T
 |
 loxP3: ATAACTTCGTATA GCATACAT TATA**C**GAAGTTAT
 1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

T **C** **T**
 | | |
 loxP23 ATA**A**ACT**T**TCGTATA GCATACAT TATA**C**GAAGTTAT
 1 2 3 4 5 6 7 8 9 10 11 12 13 13 12 11 10 9 8 7 6 5 4 3 2 1

FIGURE 14

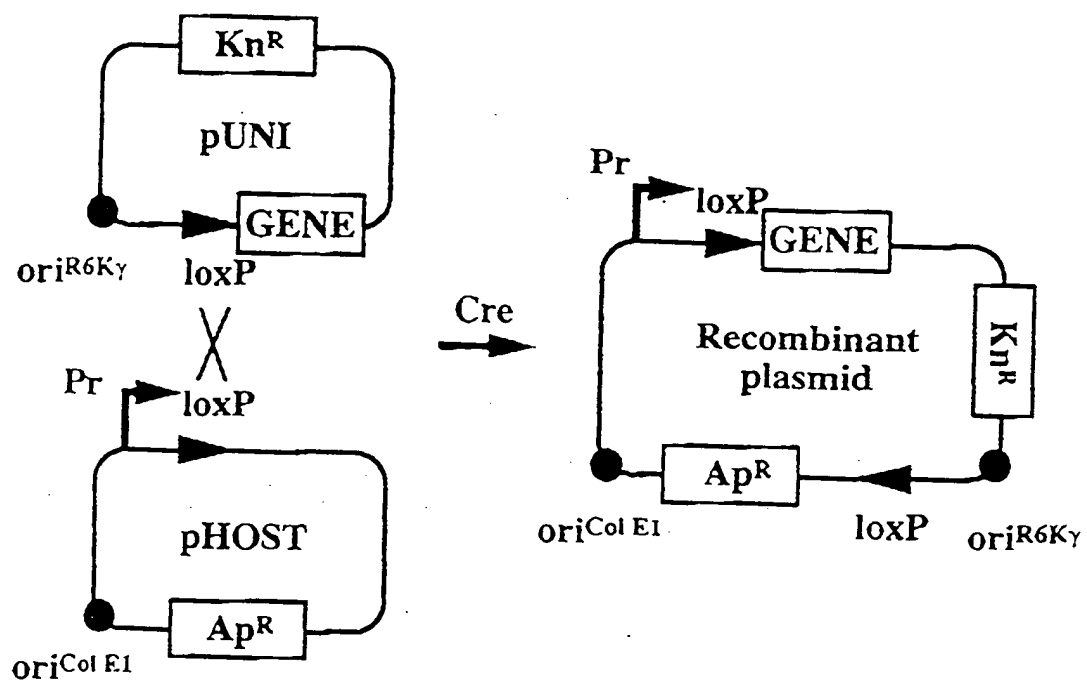


FIGURE 15

GST-Cre (μ g)	number of Ap ^R transformants	number of Kn ^R transformants	Kn ^R /Ap ^R (%)
0	4.0×10^5	0	0
0.02	3.0×10^5	231	0.1
0.04	2.3×10^5	406	0.2
0.06	2.4×10^5	868	0.4
0.08	3.3×10^5	1,336	0.4
0.10	6.0×10^4	594	1.0
0.20	7.8×10^4	580	0.7
0.40	5.8×10^4	1,910	3.3
0.60	9.2×10^4	10,750	11.7
0.80	3.1×10^5	28,660	9.2
1.00	1.0×10^5	16,840	16.8

FIGURE 16

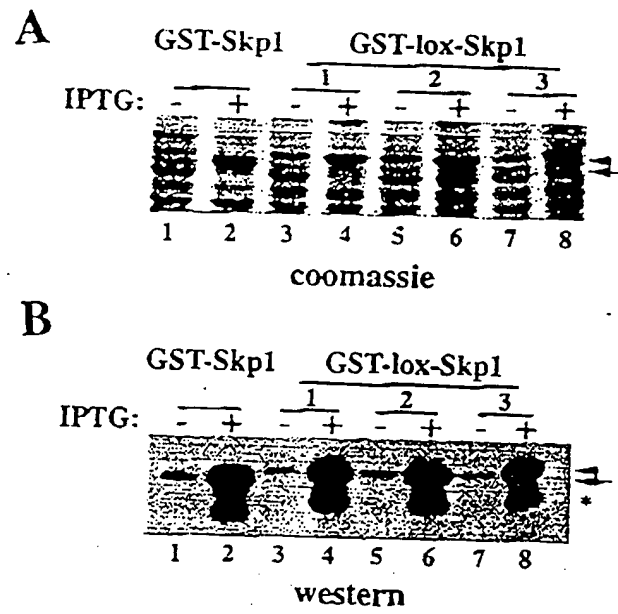


FIGURE 17

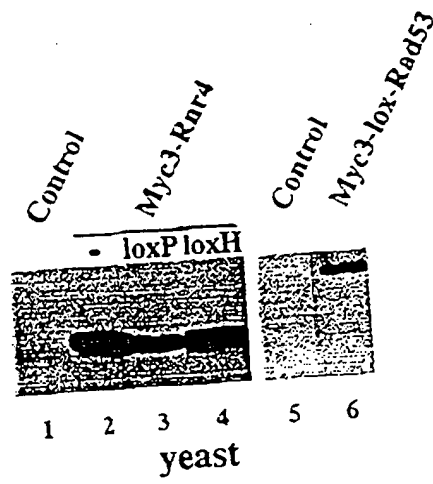


FIGURE 18

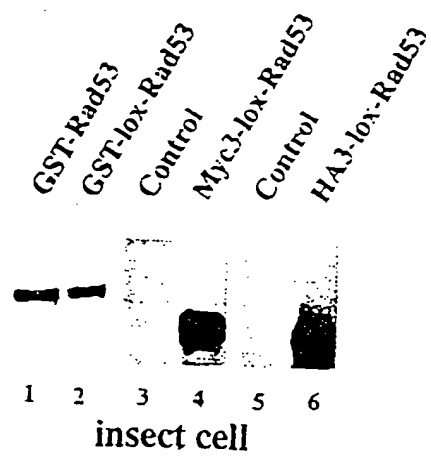


FIGURE 19

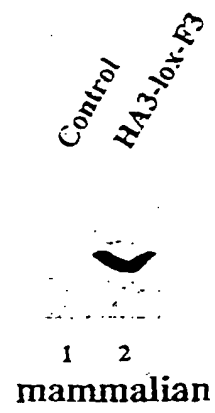


FIGURE 20

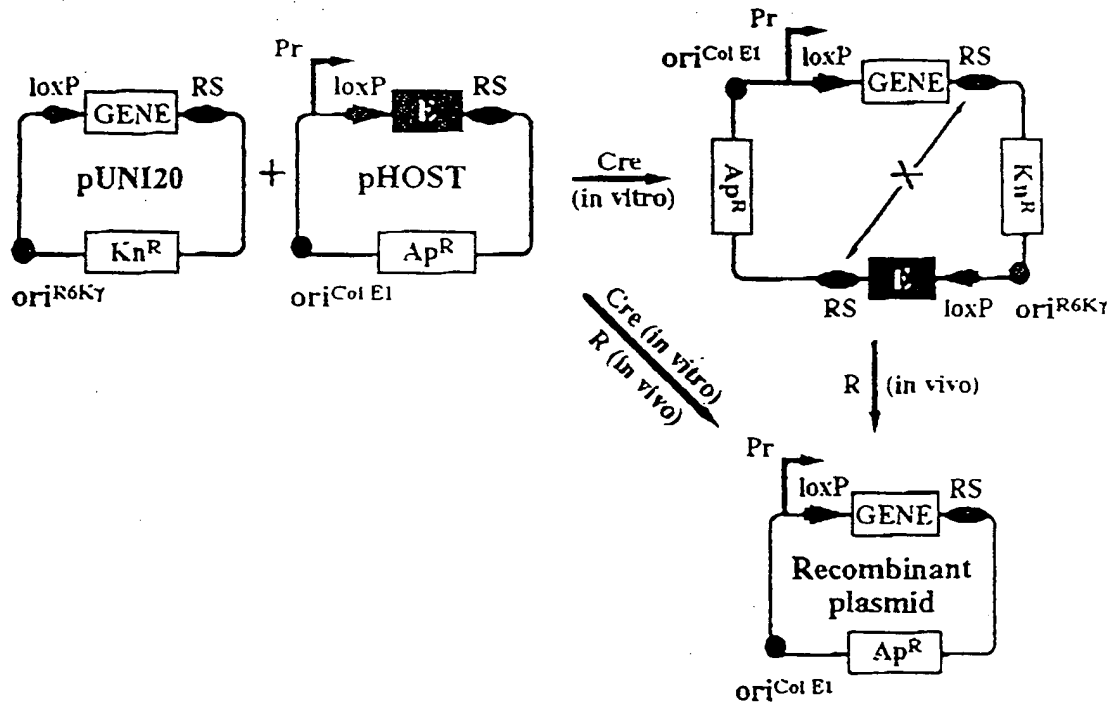


FIGURE 21

Pvu II restriction analysis of recombinant
plasmids made by one-step POT

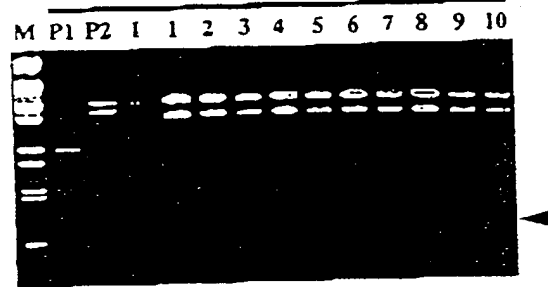
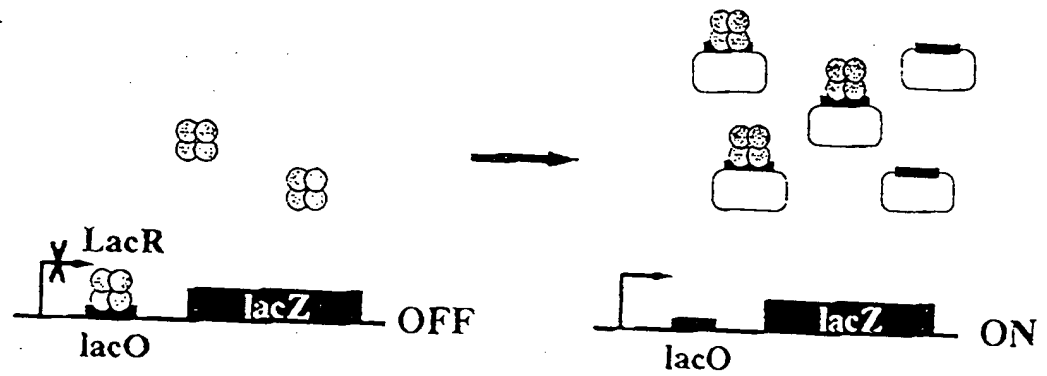
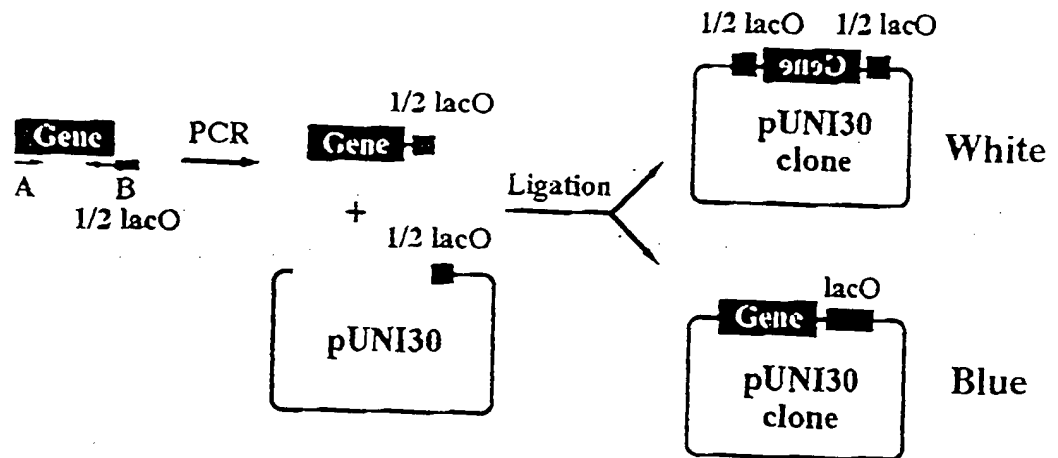


FIGURE 22

A



B



C

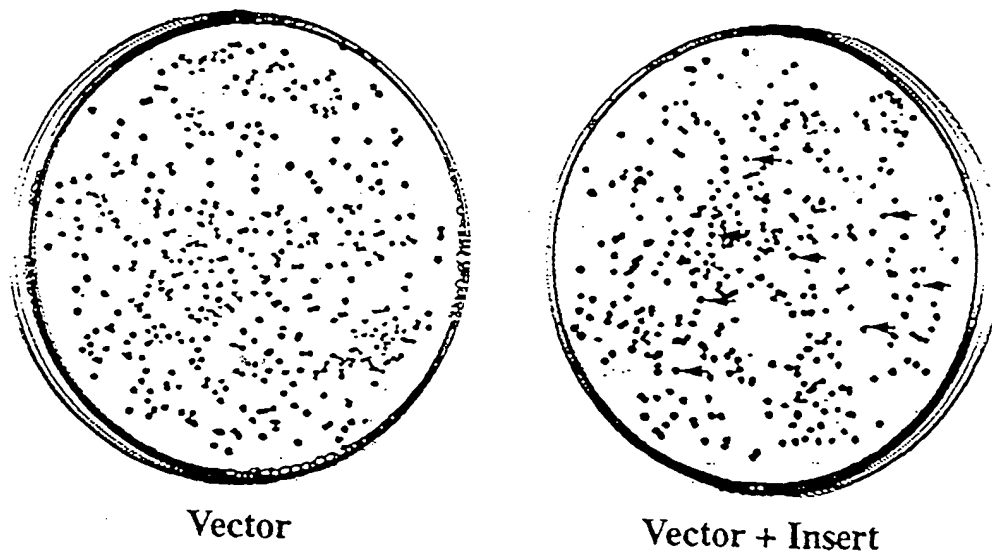
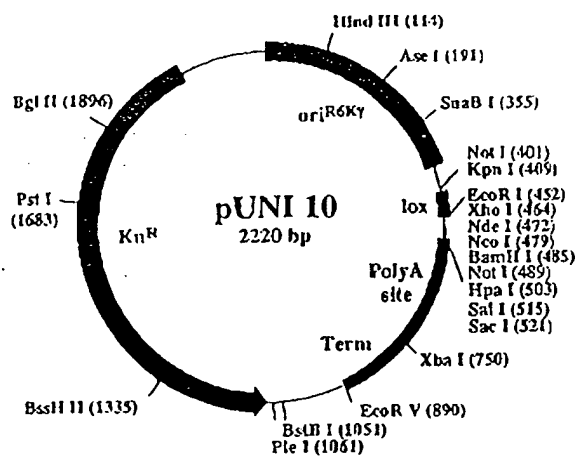


FIGURE 23

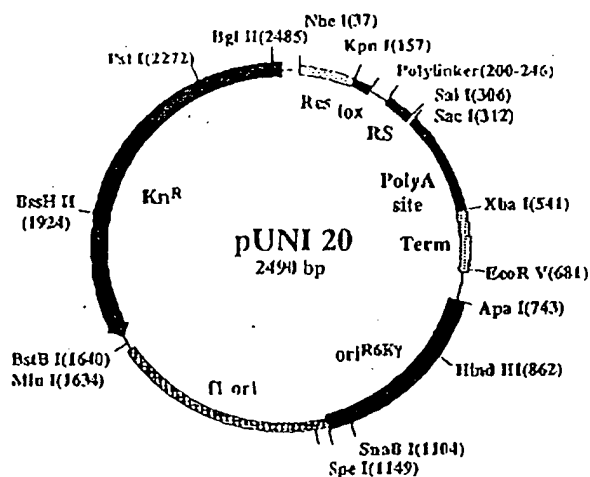


pUNI 10 Polylinker Sequence

(401) Not I KpnI LOX
 GC GGC CGC GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG A

EcoR I Sma I Xho I Nde I Nco I
 AG TTA TCT GGA ATT CCC CGG GCT CGA GAA CAT ATG GCC ATG G

BamHI Not I Hpa I Sal I Sac I (530)
 GG ATC CGC GGC CGC AAT TGT TAA CAG ATC CGT CGA CGA GCT

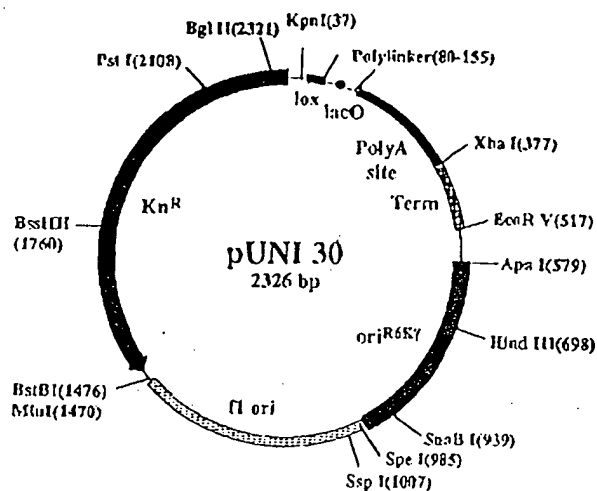


pUNI 20 Polylinker Sequence

(157) KpnI LOX
 GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA T

EcoR I Sma I Xho I Nde I Nco I BamHI
 CT GGA ATT CCC CGG GCT CGA GAACAT ATG GCC ATG GGG ATC

Not I (246)
 CGC GGC CGC



pUNI 30 Polylinker Sequence

(37) KpnI LOX
 GGT ACC ATA ACT TCG TAT AGC ATA CAT TAT ACG AAG TTA TC

EcoR I Sma I Xho I EcoRII
 T GGA ATT CCC CGG GCT CGA GCC AGT CCA GCG CTC ACA ATT
 half lacO

Not I HpaI Sal I Sac I (155)
 CGC GGC GCA ATT GTT AAC ACA TCC GTC GAC GAG CTC GC
 MluI

FIGURE 24

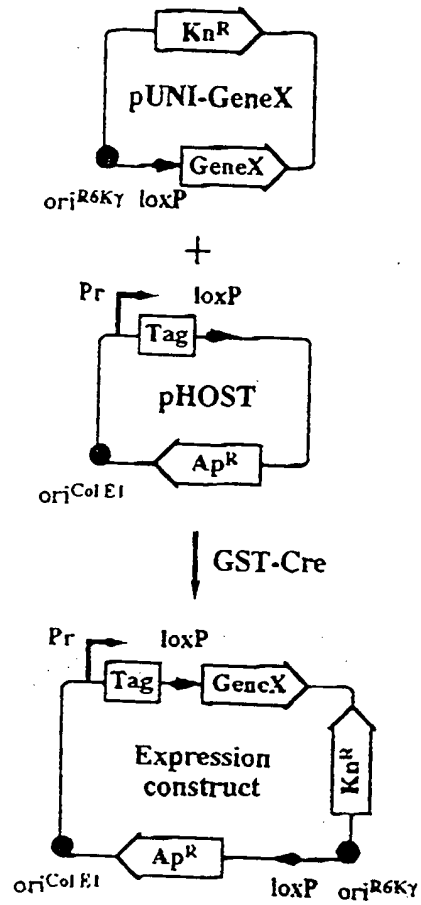


FIGURE 25

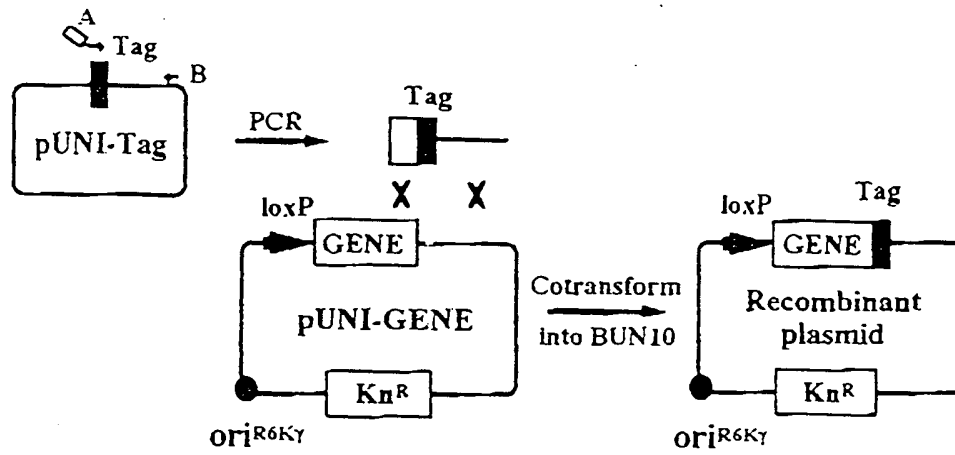


FIGURE 26A

SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCTGTCA GCCGTTAAGT GTTCCTGTGT CACTGAAAAT TGCTTTGAGA GGCTCTAAGG
60

GCTTCTCAGT GCGTTACATC CCTGGCTTGT TGTCCACAAC CGTTAAACCT TAAAAGCTTT
120

AAAAGCCTTA TATATTCTTT TTTTCTTAT AAAACTTAAA ACCTTAGAGG CTATTTAAGT
180

TGCTGATTTA TATTAATTTT ATTGTTCAAA CATGAGAGCT TAGTACGTGA AACATGAGAG
240

CTTAGTACGT TAGCCATGAG AGCTTAGTAC GTTAGCCATG AGGGTTTAGT TCGTTAAACA
300

TGAGAGCTTA GTACGTTAAA CATGAGAGCT TAGTACGTGA AACATGAGAG CTTAGTACGT
360

ACTATCAACA GGTGAACTG CTGATCAACA GATCCTCTAC GCGGCCGCGG TACCATAACT
420

TCGTATAGCA TACATTATAC GAAGTTATCT GGAATTCCCC GGGCTCGAGA ACATATGGCC
480

ATGGGGATCC GCGGCCGCAA TTGTTAACAG ATCCGTCGAC GAGCTCGCTA TCAGCCTCGA
540

CTGTGCCTTC TAGTTGCCAG CCATCTGTTG TTTGCCCCCTC CCCCCTGCCT TCCTTGACCC
600

TGGAAGGTGC CACTCCCACT GTCCTTTCCT AATAAAATGA GGAAATTGCA TCGCATTGTC
660

TGAGTAGGTG TCATTCTATT CTGGGGGGTG GGGTGGGGCA GGACAGCAAG GGGGAGGATT
720

GGGAAGACAA TAGCAGGCAT GCTGGGGATT CTAGAAGATC CGGCTGCTAA CAAAGCCCGA
780

AAGGAAGCTG AGTTGGCTGC TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC
840

TCTAAACGGG TCTTGAGGGG TTTTTTGCTG AAAGGAGGAA CTATATCCGG ATATCCCGGG
900

GTGGGCGAAG AACTCCAGCA TGAGATCCCC GCGCTGGAGG ATCATCCAGC CGGCGTCCCC
960

GAAAACGATT CCGAAGCCCA ACCTTTCATA GAAGGCGGCG GTGGAATCGA AATCTCGTGA
1020

TGGCAGGTTG GCGTTCGCTT GGTCCGTCAT TTCGAACCCC AGAGTCCCGC TCAGAAGAAC
1080

TCGTCAAGAA GGCATAGAA GGCATGCGC TCGAATCGG GAGCGGCGAT ACCGTAAAGC
 1140

ACGAGGAAGC GGTCAGCCCA TTCGCCGCCA AGCTCTTCAG CAATATCACG GGTAGCCAAC
 1200

GCTATGTCCT GATAGCGGTC CGCCACACCC AGCCGGCCAC AGTCGATGAA TCCAGAAAAG
 1260

CGGCCATTTT CCACCATGAT ATTCGGCAAG CAGGCATCGC CATGGGTCAC GACGAGATCC
 1320

TCGCCGTCGG GCATGCGCGC CTTGAGCCTG GCGAACAGTT CGGCTGGCGC GAGCCCCTGA
 1380

TGCTCTTCGT CCAGATCATC CTGATCGACA AGACCGGCTT CCATCCGAGT ACGTGCTCGC
 1440

TCGATGCGAT GTTTCGCTTG GTGGTCGAAT GGGCAGGTAG CCGGATCAAG CGTATGCAGC
 1500

CGCCGCATTG CATCAGCCAT GATGGATACT TTCTCGGCAG GAGCAAGGTG AGATGACAGG
 1560

AGATCCTGCC CCGGCACTTC GCCCAATAGC AGCCAGTCCC TTCCCGCTTC AGTGACAACG
 1620

TCGAGCACAG CTGCGCAAGG AACGCCCCTC GTGGCCAGCC ACGATAGCCG CGCTGCCTCG
 1680

TCCTGCAGTT CATTGAGGGC ACCGGACAGG TCGGTCTTGA CAAAAGAAGC CGGGCGCCCC
 1740

TGCGCTGACA GCCGGAACAC GGCGGCATCA GAGCAGCCGA TTGTCTGTTG TGCCCAGTCA
 1800

TAGCCGAATA GCCTCTCCAC CCAAGCGGCC GGAGAACCTG CGTGCAATCC ATCTTGTTCA
 1860

ATCATGCGAA ACGATCCTCA TCCTGTCTCT TGATCAGATC TTGATCCCCT GCGCCATCAG
 1920

ATCCTTGGCG GCAAGAAAGC CATCCAGTTT ACTTTGCAGG GCTTCCCAAC CTTACCAGAG
 1980

GGCGCCCCAG CTGGCAATTC CGGTTCGCTT GCTGTCCATA AAACCGCCCA GTCTAGCTAT
 2040

CGCCATGTAA GCCCACTGCA AGCTACCTGC TTTCTCTTTG CGCTTGCGTT TTCCCTTGTC
 2100

CAGATAGCCC AGTAGCTGAC ATTCATCCGG GGTCAGCACC GTTCTGCGG ACTGGCTTTC
2160

TACGTGTTCC GCTTCCTTTA GCAGCCCTTG CGCCTGAGT GCTTGCGGCA GCGTGAAGCT
2220

FIGURE 26B

SEQUENCE DESCRIPTION: SEQ ID NO:10:

48	ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC
Met	Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1	5 10 15
96	ACT CGA CTT CTT TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG
Thr	Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
	20 25 30
144	TAT GAG CGC GAT GAA GGT GAT AAA TGG CGA AAC AAA AAG TTT GAA TTG
Tyr	Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
	35 40 45
192	GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT GGT GAT GTT AAA
Gly	Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
	50 55 60
240	TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC
Leu	Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
	65 70 75 80
288	ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA
Met	Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
	85 90 95
336	GGA GCG GTT TTG GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT
Gly	Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
	100 105 110
384	AAA GAC TTT GAA ACT CTC AAA GTT GAT TTT CTT AGC AAG CTA CCT GAA
Lys	Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
	115 120 125
432	ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA ACA TAT TTA AAT
Met	Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
	130 135 140
480	GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT
Gly	Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
	145 150 155 160

GTT 528	GTT	TTA	TAC	ATG	GAC	CCA	ATG	TGC	CTG	GAT	GCG	TTC	CCA	AAA	TTA	
Val	Val	Leu	Tyr	Met 165	Asp	Pro	Met	Cys 170	Leu	Asp	Ala	Phe	Pro	Lys 175	Leu	
GTT 576	TGT	TTT	AAA	AAA	CGT	ATT	GAA	GCT	ATC	CCA	CAA	ATT	GAT	AAG	TAC	
Val	Cys	Phe	Lys 180	Lys	Arg	Ile	Glu 185	Ala	Ile	Pro	Gln	Ile	Asp 190	Lys	Tyr	
TTG 624	AAA	TCC	AGC	AAG	TAT	ATA	GCA	TGG	CCT	TTG	CAG	GGC	TGG	CAA	GCC	
Leu	Lys	Ser 195	Ser	Lys	Tyr	Ile	Ala 200	Trp	Pro	Leu	Gln	Gly 205	Trp	Gln	Ala	
ACG 672	TTT	GGT	GGT	GGC	GAC	CAT	CCT	CCA	AAA	TCG	GAT	CTG	GTT	CCG	CGT	
Thr	Phe 210	Gly	Gly	Gly	Asp	His 215	Pro	Pro	Lys	Ser	Asp 220	Leu	Val	Pro	Arg	
GGA 720	TCT	CGT	CGT	GCA	TCT	GTT	GGA	TCG	CAT	ATG	CCC	ATG	GCC	AAT	TTA	
Gly 225	Ser	Arg	Arg	Ala	Ser 230	Val	Gly	Ser	His	Met 235	Pro	Met	Ala	Asn	Leu 240	
CTG 768	ACC	GTA	CAC	CAA	AAT	TTG	CCT	GCA	TTA	CCG	GTC	GAT	GCA	ACG	AGT	
Leu	Thr	Val	His	Gln 245	Asn	Leu	Pro	Ala	Leu 250	Pro	Val	Asp	Ala	Thr 255	Ser	
GAT 816	GAG	GTT	CGC	AAG	AAC	CTG	ATG	GAC	ATG	TTC	AGG	GAT	CGC	CAG	GCG	
Asp	Glu	Val	Arg 260	Lys	Asn	Leu	Met	Asp 265	Met	Phe	Arg	Asp	Arg 270	Gln	Ala	
TTT 864	TCT	GAG	CAT	ACC	TGG	AAA	ATG	CTT	CTG	TCC	GTT	TGC	CGG	TCG	TGG	
Phe	Ser	Glu 275	His	Thr	Trp	Lys	Met 280	Leu	Leu	Ser	Val	Cys 285	Arg	Ser	Trp	
GCG 912	GCA	TGG	TGC	AAG	TTG	AAT	AAC	CGG	AAA	TGG	TTT	CCC	GCA	GAA	CCT	
Ala	Ala	Trp	Cys	Lys	Leu	Asn 295	Asn	Arg	Lys	Trp	Phe 300	Pro	Ala	Glu	Pro	
GAA 960	GAT	GTT	CGC	GAT	TAT	CTT	CTA	TAT	CTT	CAG	GCG	CGC	GGT	CTG	GCA	
Glu 305	Asp	Val	Arg	Asp	Tyr 310	Leu	Leu	Tyr	Leu	Gln 315	Ala	Arg	Gly	Leu	Ala 320	
GTA 1008	AAA	ACT	ATC	CAG	CAA	CAT	TTG	GGC	CAG	CTA	AAC	ATG	CTT	CAT	CGT	
Val	Lys	Thr	Ile	Gln 325	Gln	His	Leu	Gly	Gln 330	Leu	Asn	Met	Leu	His 335	Arg	
CGG 1056	TCC	GGG	CTG	CCA	CGA	CCA	AGT	GAC	AGC	AAT	GCT	GTT	TCA	CTG	GTT	
Arg	Ser	Gly	Leu 340	Pro	Arg	Pro	Ser	Asp 345	Ser	Asn	Ala	Val	Ser	Leu	Val	

ATG CGG CGG ATC CGA AAA GAA AAC GTT GAT GCC GGT GAA CGT GCA AAA
 1104
 Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala Lys
 355 360 365

CAG GCT CTA GCG TTC GAA CGC ACT GAT TTC GAC CAG GTT CGT TCA CTC
 1152
 Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser Leu
 370 375 380

ATG GAA AAT AGC GAT CGC TGC CAG GAT ATA CGT AAT CTG GCA TTT CTG
 1200
 Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe Leu
 385 390 395 400

GGG ATT GCT TAT AAC ACC CTG TTA CGT ATA GCC GAA ATT GCC AGG ATC
 1248
 Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg Ile
 405 410 415

AGG GTT AAA GAT ATC TCA CGT ACT GAC GGT GGG AGA ATG TTA ATC CAT
 1296
 Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile His
 420 425 430

ATT GGC AGA ACG AAA ACG CTG GTT AGC ACC GCA GGT GTA GAG AAG GCA
 1344
 Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys Ala
 435 440 445

CTT AGC CTG GGG GTA ACT AAA CTG GTC GAG CGA TGG ATT TCC GTC TCT
 1392
 Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val Ser
 450 455 460

GGT GTA GCT GAT GAT CCG AAT AAC TAC CTG TTT TGC CGG GTC AGA AAA
 1440
 Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg Lys
 465 470 475 480

AAT GGT GTT GCC GCG CCA TCT GCC ACC AGC CAG CTA TCA ACT CGC GCC
 1488
 Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg Ala
 485 490 495

CTG GAA GGG ATT TTT GAA GCA ACT CAT CGA TTG ATT TAC GGC GCT AAG
 1536
 Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala Lys
 500 505 510

GAT GAC TCT GGT CAG AGA TAC CTG GCC TGG TCT GGA CAC AGT GCC CGT
 1584
 Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala Arg
 515 520 525

GTC GGA GCC GCG CGA GAT ATG GCC CGC GCT GGA GTT TCA ATA CCG GAG
 1632
 Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro Glu
 530 535 540

ATC ATG CAA GCT GGT GGC TGG ACC AAT GTA AAT ATT GTC ATG AAC TAT
1680
Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn Tyr
545 550 555 560

ATC CGT AAC CTG GAT AGT GAA ACA GGG GCA ATG GTG CGC CTG CTG GAA
1728
Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu Glu
565 570 575

GAT GGC GAT TAG
1740
Asp Gly Asp

FIGURE 26C

SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	1	5	10	15
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	20	25	30	
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	35	40	45	
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	50	55	60	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	65	70	75	80
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	85	90	95	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	100	105	110	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	115	120	125	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	130	135	140	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	145	150	155	160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	165	170	175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	180	185	190	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	195	200	205	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	210	215	220	
Gly	Ser	Arg	Arg	Ala	Ser	Val	Gly	Ser	His	Met	Pro	Met	Ala	Asn	Leu	225	230	235	240
Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val	Asp	Ala	Thr	Ser	245	250	255	
Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	Asp	Arg	Gln	Ala	260	265	270	
Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	Cys	Arg	Ser	Trp				

275					280					285					
Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	Pro	Ala	Glu	Pro
290						295					300				
Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	Arg	Gly	Leu	Ala
305				310						315					320
Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	Met	Leu	His	Arg
				325					330					335	
Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	Val	Ser	Leu	Val
			340					345					350		
Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	Glu	Arg	Ala	Lys
							360					365			
Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	Val	Arg	Ser	Leu
	370					375					380				
Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	Leu	Ala	Phe	Leu
385				390						395					400
Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	Ile	Ala	Arg	Ile
				405					410					415	
Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	Met	Leu	Ile	His
			420					425					430		
Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	Val	Glu	Lys	Ala
		435					440					445			
Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	Ile	Ser	Val	Ser
	450					455					460				
Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	Arg	Val	Arg	Lys
465					470					475					480
Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	Ser	Thr	Arg	Ala
				485					490					495	
Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	Tyr	Gly	Ala	Lys
			500					505					510		
Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	His	Ser	Ala	Arg
		515					520					525			
Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	Ser	Ile	Pro	Glu
	530					535					540				
Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	Val	Met	Asn	Tyr
545					550					555					560
Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	Arg	Leu	Leu	Glu
				565					570					575	
Asp	Gly	Asp													